

PAGE: 1

RAW SEQUENCE LISTING

PATENT APPLICATION US/09/292,862

 DATE: 04/28/1999
 TIME: 11:33:10

Input Set: I292862.RAW

This Raw Listing contains the General Information
 Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Walter, Michael A.
2      Jordan, Tim
3      Raymond, Vincent
4  <120> TITLE OF INVENTION: NOVEL MUTATIONS IN THE FREAC3 GENE FOR
5      DIAGNOSIS AND PROGNOSIS OF GLAUCOMA AND ANTERIOR SEGMENT
6      DYSGENESIS
7  <130> FILE REFERENCE: 07540/020003
8  <140> CURRENT APPLICATION NUMBER: US/09/292,862
9  <141> CURRENT FILING DATE: 1999-04-16
10 <150> EARLIER APPLICATION NUMBER: 60/084,784
11 <151> EARLIER FILING DATE: 1998-05-08
12 <150> EARLIER APPLICATION NUMBER: 60/082,206
13 <151> EARLIER FILING DATE: 1998-04-17
14 <160> NUMBER OF SEQ ID NOS: 6
15 <170> SOFTWARE: FastSEQ for Windows Version 3.0
16 <210> SEQ ID NO 1
17 <211> LENGTH: 1662
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
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22      ggcgagcaga gctactaccg cgcgcgggcc gcggcgcccg ggggcggcta caccgccatg      120
23      ccggccccc ttagcggtga ctgcaccct gcgcacgcgc agcagtaacc gggcgccatg      180
24      gcccgcgcct acggggcccta cagcgccgag ccgcagccca aggacatggt gaagccgccc      240
25      tatagctaca tcgcgctcat caccatggcc atccagaacg ccccggaaca gaagatcacc      300
26      ctgaacggca tctaccagtt catcatggac cgcttcccct tctaccggga caacaagcag      360
27      ggctggcaga acagcatccg ccacaacctc tcgctcaacg agtgcttcgt caaggtgccg      420
28      cgcgacgaca agaagccggg caagggcagc tactggacgc tggacccgga ctccataaac      480
29      atgttcgaga acggcagctt cctgcggcgg cggcggcgct tcaagaagaa ggacgcgttg      540
30      aaggacaagg aggagaagga caggctgcac ctcaaggagc cgcccccgcc cggcgccagc      600
31      ccccgcccg cgccgccgga gcaggccgac ggcaacgcgc cgggtccgca gccgccgccc      660
32      gtgcgcatcc aggacatcaa gaccgagaac ggtacgtgcc cctcgccgcc ccagcccctg      720
33      tccccggcgc cgcccttggg cagcggcagc gccgcgcggg tgcccaagat cgagagcccc      780
34      gacagcagca gcagcagcct gtccagcggg agcagcccc cgggcagcct gccgtcggcg      840
35      cggccgctca gcctggacgg tgcggattcc gcgccgcgcg cggccgcgcc ctccgccccg      900
36      ccgccgcacc atagccaggg cttcagcgtg gacaacatca tgacgtcgct gcgggggtcg      960
37      ccgcagagcg cggccgcgga gctcagctcc ggccttcttg cctcggcggc cgctcctcg      1020
38      cgcgcgggga tcgcaccccc gctggcgctc ggcgccctact cggccggcca gagtcctctc      1080
39      tacagctccc cctgcagcca gacctccagc gcgggcagct cgggcggcgg cggcggcggc      1140
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41      agcctgtacg cggcggcgga gcgcgggggc cacttgacag gcgcgcccgg gggcgcgggc      1260
42      ggctcggccg tggacgaccc cctgcccgcg tactctctgc ctccggtcac cagcagcagc      1320
43      tcgtcgtccc tgagtcacgg cggcggcggc ggcggcgcg ggggaggcca ggaggccggc      1380
44      caccaccctg cgggccacca aggcgcgcct acctcgtggt acctgaacca ggcgggcgga      1440
  
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PAGE: 2

RAW SEQUENCE LISTING PATENT APPLICATION US/09/292,862

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45      gacctggggcc acttggcgag cgcggcgggcg gcggcgggcg cgcaggcta cccggggccag      1500
46      cagcagaact tccactcggg gcgggagatg ttcgagtcac agaggatcgg cttgaacaac      1560
47      tctccagtga acgggaatag tagctgtcaa atggccttcc cttccagcca gtctctgtac      1620
48      cgcacgtccg gagctttcgt ctacgactgt agcaagtttt ga      1662
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50      <211> LENGTH: 553
51      <212> TYPE: PRT
52      <213> ORGANISM: Homo sapiens
53      <400> SEQUENCE: 2
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55      1              5              10              15
56      Pro Tyr Leu Gly Gly Glu Gln Ser Tyr Tyr Arg Ala Ala Ala Ala Ala
57      20              25              30
58      Ala Gly Gly Gly Tyr Thr Ala Met Pro Ala Pro Met Ser Val Tyr Ser
59      35              40              45
60      His Pro Ala His Ala Glu Gln Tyr Pro Gly Gly Met Ala Arg Ala Tyr
61      50              55              60
62      Gly Pro Tyr Thr Pro Gln Pro Gln Pro Lys Asp Met Val Lys Pro Pro
63      65              70              75              80
64      Tyr Ser Tyr Ile Ala Leu Ile Thr Met Ala Ile Gln Asn Ala Pro Asp
65      85              90              95
66      Lys Lys Ile Thr Leu Asn Gly Ile Tyr Gln Phe Ile Met Asp Arg Phe
67      100             105             110
68      Pro Phe Tyr Arg Asp Asn Lys Gln Gly Trp Gln Asn Ser Ile Arg His
69      115             120             125
70      Asn Leu Ser Leu Asn Glu Cys Phe Val Lys Val Pro Arg Asp Asp Lys
71      130             135             140
72      Lys Pro Gly Lys Gly Ser Tyr Trp Thr Leu Asp Pro Asp Ser Tyr Asn
73      145             150             155             160
74      Met Phe Glu Asn Gly Ser Phe Leu Arg Arg Arg Arg Arg Phe Lys Lys
75      165             170             175
76      Lys Asp Ala Leu Lys Asp Lys Glu Glu Lys Asp Arg Leu His Leu Lys
77      180             185             190
78      Glu Pro Pro Pro Pro Gly Ala Ser Pro Arg Pro Ala Pro Pro Glu Gln
79      195             200             205
80      Ala Asp Gly Asn Ala Pro Gly Pro Gln Pro Pro Pro Val Arg Ile Gln
81      210             215             220
82      Asp Ile Lys Thr Glu Asn Gly Thr Cys Pro Ser Pro Pro Gln Pro Leu
83      225             230             235             240
84      Ser Pro Ala Ala Ala Leu Gly Ser Gly Ser Ala Ala Ala Val Pro Lys
85      245             250             255
86      Ile Glu Ser Pro Asp Ser Ser Ser Ser Ser Leu Ser Ser Gly Ser Ser
87      260             265             270
88      Pro Pro Gly Ser Leu Pro Ser Ala Arg Pro Leu Ser Leu Asp Gly Ala
89      275             280             285
90      Asp Ser Ala Pro Pro Pro Pro Ala Pro Ser Ala Pro Pro Pro His His
91      290             295             300
92      Ser Gln Gly Phe Ser Val Asp Asn Ile Met Thr Ser Leu Arg Gly Ser
93      305             310             315             320
94      Pro Gln Ser Ala Ala Ala Glu Leu Ser Ser Gly Leu Leu Ala Ser Ala

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PAGE: 3

RAW SEQUENCE LISTING PATENT APPLICATION US/09/292,862

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95              325              330              335
96  Ala Ala Ser Ser Arg Ala Gly Ile Ala Pro Pro Leu Ala Leu Gly Ala
97              340              345              350
98  Tyr Ser Pro Gly Gln Ser Ser Leu Tyr Ser Ser Pro Cys Ser Gln Thr
99              355              360              365
100 Ser Ser Ala Gly Ser Ser Gly Gly Gly Gly Gly Gly Ala Gly Ala Ala
101              370              375              380
102 Gly Gly Ala Gly Gly Ala Gly Thr Tyr His Cys Asn Leu Gln Ala Met
103              385              390              395              400
104 Ser Leu Tyr Ala Ala Gly Glu Arg Gly Gly His Leu Gln Gly Ala Pro
105              405              410              415
106 Gly Gly Ala Gly Gly Ser Ala Val Asp Asp Pro Leu Pro Asp Tyr Ser
107              420              425              430
108 Leu Pro Pro Val Thr Ser Ser Ser Ser Ser Ser Leu Ser His Gly Gly
109              435              440              445
110 Gly Gly Gly Gly Gly Gly Gly Gly Gln Glu Ala Gly His His Pro Ala
111              450              455              460
112 Ala His Gln Gly Arg Leu Thr Ser Trp Tyr Leu Asn Gln Ala Gly Gly
113              465              470              475              480
114 Asp Leu Gly His Leu Ala Ser Ala Ala Ala Ala Ala Ala Ala Gly
115              485              490              495
116 Tyr Pro Gly Gln Gln Gln Asn Phe His Ser Val Arg Glu Met Phe Glu
117              500              505              510
118 Ser Gln Arg Ile Gly Leu Asn Asn Ser Pro Val Asn Gly Asn Ser Ser
119              515              520              525
120 Cys Gln Met Ala Phe Pro Ser Ser Gln Ser Leu Tyr Arg Thr Ser Gly
121              530              535              540
122 Ala Phe Val Tyr Asp Cys Ser Lys Phe
123              545              550
124 <210> SEQ ID NO 3
125 <211> LENGTH: 12
126 <212> TYPE: DNA
127 <213> ORGANISM: Homo sapiens
128 <400> SEQUENCE: 3
129      agtaaataaa ca
130 <210> SEQ ID NO 4
131 <211> LENGTH: 12
132 <212> TYPE: DNA
133 <213> ORGANISM: Homo sapiens
134 <400> SEQUENCE: 4
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136 <210> SEQ ID NO 5
137 <211> LENGTH: 20
138 <212> TYPE: DNA
139 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 5
141      gcttcattcc gaatcaccag
142 <210> SEQ ID NO 6
143 <211> LENGTH: 20
144 <212> TYPE: DNA

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12

12

20

PAGE: 4

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DATE: 04/28/1999
TIME: 11:33:10

Input Set: I292862.RAW

145 <213> ORGANISM: Homo sapiens
146 <400> SEQUENCE: 6
147 gtcccctccc tccaactatc

20

PAGE: 5

VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
